NOVEL MURINE POLYNUCLEOTIDE SEQUENCES AND MUTANT CELLS AND MUTANT ANIMALS DEFINED THEREBY

The present application claims priority to U.S. Provisional Appl. Ser. No. 60/237,272 which was filed October 2, 2000. The present application incorporates by reference U.S. Applications Ser. No. 08/728,963, 60/109,302, 09/276,533 and U.S. Patent Numbers 6,080,576, 6,136,566, 6,139,833 and their respective disclosures in their entirety.

1.0. FIELD OF THE INVENTION

The present invention is in the field of molecular genetics. The application discloses novel nucleic acid sequences that: each define the locus of a corresponding mutated murine embryonic stem cell clone; partially define the scope of exons that can be trapped and identified by the disclosed vectors/methods; and that are also useful, *inter alia*, for identifying the coding regions of the murine genome.

2.0. BACKGROUND OF THE INVENTION

Most mammalian genes are divided into exons and introns. Exons are the portions of the gene that are spliced into mRNA and encode the protein product of a gene. In genomic DNA, these coding exons are divided by non-coding intron sequences. Although RNA polymerase transcribes both intron and exon sequences, the intron sequences must be removed from the transcript so that the resulting mRNA can be translated into protein. Accordingly, all mammalian, and most eukaryotic, cells have the machinery to splice exons into mRNA.

Gene trap vectors have been designed to integrate into introns or genes in a manner that allows the cellular splicing machinery to splice vector encoded exons to cellular mRNAs. Commonly, gene trap vectors contain selectable marker sequences that are preceded by strong splice acceptor sequences and are not preceded by a promoter. Thus, when such vectors integrate into a gene, the cellular splicing machinery splices exons from the trapped gene onto the 5' end of the selectable marker sequence. Typically, such selectable marker